SEQUENCE LISTING

<110> Lukyanov, Sergey

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<170> PatentIn version 3.1

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<213> Pontellina plumata

<400> 1

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<210> 2

<211> 222

<212> PRT

<213> Pontellina plumata

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Val Val Phe Glu Leu Val Gly Gly Gly Glu Gly Ile Pro Glu Gln Gly
                20                  25                  30
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        35              40              45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
        50              55              60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ala Asn Asn
65              70              75              80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
                85              90              95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
            100             105             110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
        115             120             125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
        130             135             140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145             150             155             160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
                165             170             175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Ser Met Phe
            180             185             190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
            195             200             205
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<213> Pontellina plumata
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<213> Pontellina plumata
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                20   25   30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
            35   40   45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
        50   55   60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65   70   75   80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
                85   90   95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
                100   105   110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
            115   120   125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
        130   135   140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145   150   155   160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
                165   170   175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
                180   185   190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
            195   200   205
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Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
    210             215             220

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<212>   DNA
<213>   Labidocera aestiva

<400>   5

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cagaacggag gatccatgtt tacctacagg aaggttgagg agctccacag ccagtcagat   660
gttggtattg tagaatacca acatgtcttc aagaccccaa ctgcttttgc ctaagcttgg   720
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<210>   6
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<212>   PRT
<213>   Labidocera aestiva

<400>   6

Met Pro Val Met Lys Ile Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
1   5   10   15
Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
                20   25   30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
            35   40   45
Pro Tyr Leu Leu Ser His Ile Met Gly Tyr Gly Phe Tyr His Tyr Ala
        50   55   60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Ala Lys Asn
65   70   75   80

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Gly Gly Tyr Thr Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
            85                  90                  95
Ile Ser Val Asn Phe Thr Tyr Arg Tyr Glu Gly Asn Lys Val Ile Gly
            100                 105                 110
Asp Phe Lys Val Val Gly Ser Gly Phe Pro Ala Asn Ser Val Ile Phe
            115                 120                 125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
            130                 135                 140
Lys Gly Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145                 150                 155                 160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Leu His Phe
            165                 170                 175
Lys Thr Ala Met His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
            180                 185                 190
Thr Tyr Arg Lys Val Glu Glu Leu His Ser Gln Ser Asp Val Gly Ile
            195                 200                 205
Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
    210                 215                 220
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<211>  753
<212>  DNA
<213>  cf. Pontella meadi Wheeler
<400>  7
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atacagatga gggacgcatg accaacaaaa tgaagtccat caaaggacct atctccttct   180
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atactcttgt gaatgcctac accagaacat atttgcttaa agatggtgga tactactctg   540
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<210>  8
<211>  222
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<212>   PRT
<213>   cf. Pontella meadi Wheeler
<400>   8

Met Pro Asp Met Lys Leu Glu Cys His Ile Ser Gly Thr Met Asn Gly
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Glu Glu Phe Glu Leu Ile Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
            20   25   30
Arg Met Thr Asn Lys Met Lys Ser Ile Lys Gly Pro Ile Ser Phe Ser
        35   40   45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
    50   55   60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65   70   75   80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
                85   90   95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Asn Lys Ile Ile Gly
            100   105   110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Thr Asn Ser Leu Ile Phe
        115   120   125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
    130   135   140
Lys Ala Asp Asn Thr Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
145   150   155   160
Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
                165   170   175
Lys Ser Ala Ile His Thr Thr Met Leu Gln Asn Gly Gly Ser Met Phe
            180   185   190
Thr Tyr Arg Val Val Glu Glu Thr His Thr Gln Asn Glu Val Ala Ile
        195   200   205
Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
    210   215   220

<210>   9
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<212>   DNA
<213>   cf. Pontella meadi Wheeler
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agaatggagg ttactcaaat gtcaggactg agaggtatga ggatggaggc atcatttcta    420
taaccttcaa ctacagatat gaaggcagca agatcattgg agacttcaaa gttattggaa    480
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ccatccatcc tacaatgctc cagaatggtg gatccatgtt cactcacaga gtagtagagg    720
agaaccacac taagaccaac gttgctatcg tagagtacca aaatgtcttc aaaactccta    780
ctgcatttgc ttaaaatact tgtaacaaaa ctgcaagaa ataacctata ttgtacaata    840
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<210>  10
<211>  222
<212>  PRT
<213>  cf. Pontella meadi Wheeler
<400>  10
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Glu Glu Phe Glu Leu Ile Gly Ser Gly Asp Gly Asn Thr Asp Gln Gly
            20                  25                  30
Arg Met Thr Asn Asn Met Lys Ser Ile Lys Gly Pro Leu Ser Phe Ser
        35                  40                  45
Pro Tyr Leu Leu Ser His Ile Leu Gly Tyr Gly Tyr Tyr His Phe Ala
    50                  55                  60
Thr Phe Pro Ala Gly Tyr Glu Asn Ile Tyr Leu His Ala Met Lys Asn
65                  70                  75                  80
Gly Gly Tyr Ser Asn Val Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
                85                  90                  95
Ile Ser Ile Thr Phe Asn Tyr Arg Tyr Glu Gly Ser Lys Ile Ile Gly
                100                 105                 110
Asp Phe Lys Val Ile Gly Thr Gly Phe Pro Thr Asp Ser Leu Ile Phe
            115                 120                 125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu Asn Met Phe Pro
            130                 135                 140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Tyr Leu Leu
145                 150                 155                 160
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Lys Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
                165                 170             175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
                180                 185             190
Thr His Arg Val Val Glu Glu Asn His Thr Lys Thr Asn Val Ala Ile
            195                 200             205
Val Glu Tyr Gln Asn Val Phe Lys Thr Pro Thr Ala Phe Ala
    210                 215             220
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<210> 11
<211> 847
<212> DNA
<213> Pontella mediterranea
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tttgaacttg ttggtgctgg agaaggaaac actgatgagg acgcatgac  caacaagatg     180
aagtccacca agggacctct ttccttctct ccttatttgc tctcccacgt tcttggttat     240
ggatactacc actatgctac cttccctgct ggatatgaaa atgtctacct ccatgccatg     300
aagaatggag gttactccaa cacaagaact gagaggtatg aggatggagg tatcatttct     360
gctaccttca actacagata tgaaggagga cagattcatg gagacttcaa ggttgtagga     420
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<213> Pontella mediterranea
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Glu Glu Phe Glu Leu Val Gly Ala Gly Glu Gly Asn Thr Asp Glu Gly
                20                  25                  30
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Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
        35              40              45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
        50              55             .60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65              70              75              80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Glu Asp Gly Gly Ile
                85              90              95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
            100             105             110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
        115             120             125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
        130             135             140
Lys Ala Asn Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145             150             · 155            160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Leu
            165             170             175
Gln Ser Ala Ile His Pro Thr Met Leu Lys Asn Gly Gly Ser Met Phe
            180             185             190
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
        195             200             205
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
        210             215             220
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<212> DNA
<213> Pontella mediterranea
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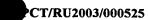gcagtggtat caacgcagag tacgcgggga gttcctcaac gaaaaccgag agaaacatac    60
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gccatccatc ccaccatgct ccagaatggt ggatctatgt tcacctacag aaaggttgag   660
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acagcttttg cttaattttg taaataaaga aagaatttat aatacaatag tgcttttatg   780
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aaaaaaaaaa                                                          850
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<212> PRT
<213> Pontella mediterranea

<400> 14

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Met Pro His Met Lys Leu Glu Cys Arg Ile Ser Gly Thr Met Asn Gly
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Glu Glu Phe Glu Leu Val Gly Ala Gly Asp Gly Asn Thr Asp Glu Gly
                20                  25                  30
Arg Met Thr Asn Gln Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
        35                  40                  45
Pro Tyr Leu Leu Ser His Val Leu Gly Tyr Gly Tyr Tyr His Tyr Ala
    50                  55                  60
Thr Phe Pro Ala Gly Tyr Glu Asn Val Tyr Leu His Ala Met Lys Asn
65                  70                  75                  80
Gly Gly Tyr Ser Asn Thr Arg Thr Glu Arg Tyr Asp Asp Gly Gly Ile
                85                  90                  95
Ile Ser Ala Thr Phe Asn Tyr Arg Tyr Glu Gly Arg Gln Ile His Gly
            100                 105                 110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Ala Asp Ser Ile Ile Phe
            115                 120                 125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Thr Cys Glu His Ile Tyr Pro
        130                 135                 140
Lys Ala Asp Asn Ile Leu Val Asn Ala Tyr Thr Arg Thr Trp Met Leu
145                 150                 155                 160
Arg Asp Gly Gly Tyr Tyr Ser Ala Gln Val Asn Asn His Met His Phe
                165                 170                 175
Lys Ser Ala Ile His Pro Thr Met Leu Gln Asn Gly Gly Ser Met Phe
            180                 185                 190
Thr Tyr Arg Lys Val Glu Glu Leu His Thr Gln Thr Glu Val Gly Ile
            195                 200                 205
Val Glu Tyr Gln His Val Phe Lys Arg Pro Thr Ala Phe Ala
        210                 215                 220
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<210> 15
<211> 821
<212> DNA
<213> Unknown
<220>
<223> nucleic acid sequence for pdae1GFP from an unidentified
      Pontellidae species, complete cds
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ggaaatactg atcagggacg tatgaccaac aagatgaaat ctaccaaggg tccactctcc     180
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ggaaacaaga ttatcgggga cttcaagtgt gtcggaactg gattccctga ggacagcgtt     420
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tctggccagg ttaccagcca catccacttc aagaatgcga tccacccatc catccttcat     600
aacggcggat ccatgttcac ctacagaaga gttgaggagc tccacactca aactgatctt     660
ggaattgttg agtaccagca tgtattcaag actcccactg cttttgcttg aatgccatga     720
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taattctcga gaattcatat aatacataga atttatctta c                        821
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<210> 16
<211> 222
<212> PRT
<213> Unknown
<220>
<223> amino acid sequence for pdae1GFP from an unidentified Pontellidae
      species
<400> 16


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Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Asn Thr Asp Gln Gly
                20                  25                  30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Pro Leu Ser Phe Ser
            35                  40                  45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
    50                  55                  60
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Thr Phe Pro Ser Gly Tyr Glu Asn Pro Tyr Val His Ala Met Thr Asn
65   70   75   80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Ser Tyr Glu Asp Gly Gly Val
                85   90   95
Leu Tyr Leu Thr Phe Asn Tyr Arg Leu Asp Gly Asn Lys Ile Ile Gly
            100   105   110
Asp Phe Lys Cys Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
        115   120   125
Thr Asp Lys Ile Ile Lys Ser Asn Pro Asn Cys Glu His Phe Tyr Pro
        130   135   140
Met Ala Glu Asn Ile Met Lys Asn Ala Tyr Met Arg Thr Leu Ser Leu
145   150   155   160
Arg Asp Gly Gly Tyr Tyr Ser Gly Gln Val Thr Ser His Ile His Phe
                165   170   175
Lys Asn Ala Ile His Pro Ser Ile Leu His Asn Gly Gly Ser Met Phe
            180   185   190
Thr Tyr Arg Arg Val Glu Glu Leu His Thr Gln Thr Asp Leu Gly Ile
        195   200   205
Val Glu Tyr Gln His Val Phe Lys Thr Pro Thr Ala Phe Ala
        210   215   220

<210> 17
<211> 669
<212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the humanized version of the ppluGFP2
<400> 17

atgcccgcca tgaagatcga gtgccgcatc accggcaccc tgaacggcgt ggagttcgag   60
ctggtgggcg gcggagaggg cacccccgag cagggccgca tgaccaacaa gatgaagagc   120
accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc   180
taccacttcg gcacctaccc cagcggctac gagaacccct tcctgcacgc catcaacaac   240
ggcggctaca ccaacacccg catcgagaag tacgaggacg cggcgtgct gcacgtgagc   300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc   360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag   420
cacctgcacc ccatgggcga taacgtgctg gtgggcagct cgcccgcac cttcagcctg   480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc   540
cacccagca tcctgcagaa cgggggcccc atgttcgcct ccgccgcgt ggaggagctg   600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca   660
ttcgcctga   669

```
<210>  18
<211>  222
<212>  PRT
<213>  Artificial sequence
<220>
<223>  amino acid sequence for the humanized version of the ppluGFP2
<400>  18
```

```
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1               5                   10                  15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
                20              25                  30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
            35                  40                  45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
        50                  55                  60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65                  70                  75                  80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
                85                  90                  95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
                100                 105                 110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
            115                 120                 125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
        130                 135                 140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145                 150                 155                 160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
                165                 170                 175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
            180                 185                 190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
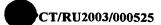        195                 200                 205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
        210                 215                 220
```

```
<210>  19
<211>  589
<212>  DNA
<213>  Artificial sequence
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<220>

<223>   nucleic acid sequence for the ppluGFP2 with yeast-optimized codon
        usage

<400>   19


```
tactccagaa caaggtagaa tgactaataa aatgaaatct actaaaggtg ctttgacttt    60
ttctccatat ttgttgtctc atgttatggg ttatggtttt tatcattttg gtacttatcc   120
atctggttat gaaaatccat ttttgcatgc tattaataat ggtggttata ctaatactag   180
aattgaaaaa tatgaagatg gtggtgtttt gcatgtttct ttttcttata gatatgaagc   240
tggtagagtt attggcgatt ttaaagttgt tggtactggt tttccagaag attctgttat   300
ttttactgat aaaattatta gatctaatgc tactgttgaa catttgcatc caatgggtga   360
taatgttttg gttggttctt ttgctagaac ttttttctttg agagatggtg gttattattc   420
ttttgttgtt gattctcata tgcattttaa atctgctatt catccatcta ttttgcaaaa   480
tggtggtcca atgtttgctt ttagaagagt tgaagaattg cattctaata ctgaattggg   540
tattgttgaa tatcaacatg ctttttaaaac tccaattgct tttgcttaa             589
```


<210>   20
<211>   222
<212>   PRT
<213>   Artificial sequence
<220>
<223>   amino acid sequence for the ppluGFP2 with yeast-optimized codon u
        sage
<400>   20


```
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1               5                   10                  15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
            20                  25                  30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
        35                  40                  45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
    50                  55                  60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65                  70                  75                  80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
                85                  90                  95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
            100                 105                 110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
        115                 120                 125
```

```
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
    130                 135             140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145                 150             155                 160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
                165             170             175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
                180             185             190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
        195             200             205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala
    210                 215             220
```

<210> 21
<211> 669
<212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the CopCFP mutant
<400> 21

```
atgcccgcca tgaagatcga gtgccgcatc accggcaccc tgaacggcgt ggagttcgag   60
ctggtgggcg gcggagaggg caccccccgag cagggccgca tgaccaacaa gatgaagagc  120
accaaaggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctggggcttt  180
taccacttcg gcacctaccc cagcggctac gagaacccct tcctgcacgc catcaacaac  240
ggcggctaca ccaacacccg catcgagaag tacgaggacg cggcgtgct gcacgtgagc  300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc  360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag  420
cacctgcgcc ccatgggcga taacgtgctg gtgggcagct cgcccgcac cttcagcctg  480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc  540
cacccccagca tcctgcagaa cggggggcccc atgttcgcct ccgccgcgt ggaggagctg  600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgaccgca  660
ttcgcctaa                                                          669
```

<210> 22
<211> 222
<212> PRT
<213> Artificial sequence
<220>
<223> amino acid sequence for the CopCFP mutant
<400> 22

```
Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1               5                   10              15
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
                20              25              30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
        35              40              45
Pro Tyr Leu Leu Ser His Val Met Gly Trp Gly Phe Tyr His Phe Gly
    50              55              60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65              70              75              80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
            85              90              95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
            100             105             110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
        115             120             125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu Arg Pro
    130             135             140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145             150             155             160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
            165             170             175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
            180             185             190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
        195             200             205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Thr Ala Phe Ala
    210             215             220
```

<210> 23
<211> 690
<212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the CopGFP-NA1 variant
<400> 23

```
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ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcacccccga gcagggccgc   120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagcccota cctgctgagc   180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc cagcggcta cgagaacccc   240
```

```
ttcctgcacg ccatcaacaa cggcggctac accaacaccc gcatcgagaa gtacgaggac   300
ggcggcgtgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac   360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc   420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc   480
ttcgcccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac   540
atgcacttca gagcgccat ccaccccagc atcctgcaga acgggggccc catgttcgcc   600
ttcgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac   660
gccttcaaga ccccgatcgc attcgcctga                                    690
```

<210> 24
<211> 229
<212> PRT
<213> Artificial sequence
<220>
<223> amino acid sequence for the CopGFP-NA1 variant
<400> 24


```
Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1               5                   10                  15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
            20                  25                  30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
            35                  40                  45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
        50                  55                  60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65                  70                  75                  80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
                85                  90                  95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
            100                 105                 110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
        115                 120                 125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
        130                 135                 140
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145                 150                 155                 160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
                165                 170                 175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
                180                 185                 190
```

Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
      195   200   205

Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
      210   215   220

Pro Ile Ala Phe Ala
225

<210> 25
<211> 819
<212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the CopGFP-NA2 variant
<400> 25

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accaagggcg ccctgacctt cagcccctac ctgctgagcc acgtgatggg ctacggcttc   180
taccacttcg gcacctaccc cagcggctac gagaaccccт tcctgcacgc catcaacaac   240
ggcggctaca ccaacacccg catcgagaag tacgaggacg cggcgtgct gcacgtgagc   300
ttcagctacc gctacgaggc cggccgcgtg atcggcgact tcaaggtggt gggcaccggc   360
ttccccgagg acagcgtgat cttcaccgac aagatcatcc gcagcaacgc caccgtggag   420
cacctgcacc ccatgggcga taacgtgctg gtgggcagct cgcccgcac cttcagcctg   480
cgcgacggcg gctactacag cttcgtggtg gacagccaca tgcacttcaa gagcgccatc   540
cacccccagca tcctgcagaa cggggggcccc atgttcgcct ccgccgcgt ggaggagctg   600
cacagcaaca ccgagctggg catcgtggag taccagcacg ccttcaagac cccgatcgca   660
ttcgccagat ccagagccca ggccagcaac tccgccgtgg atggcacagc cggaccggga   720
tcggccgcga ctctagatca taatcagcca taccacattt gtagaggttt tacttgcttt   780
aaaaaacctc ccacacctcc ccctgaacct gaaacataa   819

<210> 26
<211> 272
<212> PRT
<213> Artificial sequence
<220>
<223> amino acid sequence for the CopGFP-NA2 variant
<400> 26

Met Pro Ala Met Lys Ile Glu Cys Arg Ile Thr Gly Thr Leu Asn Gly
1   5   10   15

```
Val Glu Phe Glu Leu Val Gly Gly Gly Glu Gly Thr Pro Glu Gln Gly
                20              25              30
Arg Met Thr Asn Lys Met Lys Ser Thr Lys Gly Ala Leu Thr Phe Ser
        35              40              45
Pro Tyr Leu Leu Ser His Val Met Gly Tyr Gly Phe Tyr His Phe Gly
        50              55              60
Thr Tyr Pro Ser Gly Tyr Glu Asn Pro Phe Leu His Ala Ile Asn Asn
65              70              75              80
Gly Gly Tyr Thr Asn Thr Arg Ile Glu Lys Tyr Glu Asp Gly Gly Val
                85              90              95
Leu His Val Ser Phe Ser Tyr Arg Tyr Glu Ala Gly Arg Val Ile Gly
            100             105             110
Asp Phe Lys Val Val Gly Thr Gly Phe Pro Glu Asp Ser Val Ile Phe
        115             120             125
Thr Asp Lys Ile Ile Arg Ser Asn Ala Thr Val Glu His Leu His Pro
    130             135             140
Met Gly Asp Asn Val Leu Val Gly Ser Phe Ala Arg Thr Phe Ser Leu
145             150             155             160
Arg Asp Gly Gly Tyr Tyr Ser Phe Val Val Asp Ser His Met His Phe
                165             170             175
Lys Ser Ala Ile His Pro Ser Ile Leu Gln Asn Gly Gly Pro Met Phe
            180             185             190
Ala Phe Arg Arg Val Glu Glu Leu His Ser Asn Thr Glu Leu Gly Ile
        195             200             205
Val Glu Tyr Gln His Ala Phe Lys Thr Pro Ile Ala Phe Ala Arg Ser
    210             215             220
Arg Ala Gln Ala Ser Asn Ser Ala Val Asp Gly Thr Ala Gly Pro Gly
225             230             235             240
Ser Ala Ala Thr Leu Asp His Asn Gln Pro Tyr His Ile Cys Arg Gly
            245             250             255
Phe Thr Cys Phe Lys Lys Pro Pro Thr Pro Pro Pro Glu Pro Glu Thr
            260             265             270
```

<210> 27
<211> 840
<212> DNA
<213> Artificial sequence
<220>
<223> nucleic acid sequence for the CopGFP-NA3 variant
<400> 27
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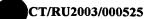ctgaacggcg tggagttcga gctggtgggc ggcggagagg gcaccccccga gcagggccgc    120
atgaccaaca agatgaagag caccaagggc gccctgacct tcagccccta cctgctgagc    180
cacgtgatgg gctacggctt ctaccacttc ggcacctacc ccagcggcta cgagaacccc    240
ttcctgcacg ccatcaacaa cggcggctac accaacaccc gcatcgagaa gtacgaggac    300
ggcggcgtgc tgcacgtgag cttcagctac cgctacgagg ccggccgcgt gatcggcgac    360
ttcaaggtgg tgggcaccgg cttccccgag gacagcgtga tcttcaccga caagatcatc    420
cgcagcaacg ccaccgtgga gcacctgcac cccatgggcg ataacgtgct ggtgggcagc    480
ttcgcccgca ccttcagcct gcgcgacggc ggctactaca gcttcgtggt ggacagccac    540
atgcacttca gagcgccat ccacccccagc atcctgcaga acggggggccc catgttcgcc    600
ttccgccgcg tggaggagct gcacagcaac accgagctgg gcatcgtgga gtaccagcac    660
gccttcaaga ccccgatcgc attcgccaga tccagagccc aggccagcaa ctccgccgtg    720
gatggcacag ccggaccggg atcggccgcg actctagatc ataatcagcc ataccacatt    780
tgtagaggtt ttacttgctt taaaaaacct cccacacctc cccctgaacc tgaaacataa    840
```

```
<210>    28
<211>    279
<212>    PRT
<213>    Artificial sequence
<220>
<223>    amino acid sequence for the CopGFP-NA3 variant
<400>    28
```

```
Met Glu Ser Asp Glu Ser Gly Leu Pro Ala Met Glu Ile Glu Cys Arg
1               5                   10                  15
Ile Thr Gly Thr Leu Asn Gly Val Glu Phe Glu Leu Val Gly Gly Gly
                20                  25                  30
Glu Gly Thr Pro Glu Gln Gly Arg Met Thr Asn Lys Met Lys Ser Thr
            35                  40                  45
Lys Gly Ala Leu Thr Phe Ser Pro Tyr Leu Leu Ser His Val Met Gly
        50                  55                  60
Tyr Gly Phe Tyr His Phe Gly Thr Tyr Pro Ser Gly Tyr Glu Asn Pro
65                  70                  75                  80
Phe Leu His Ala Ile Asn Asn Gly Gly Tyr Thr Asn Thr Arg Ile Glu
                85                  90                  95
Lys Tyr Glu Asp Gly Gly Val Leu His Val Ser Phe Ser Tyr Arg Tyr
                100                 105                 110
Glu Ala Gly Arg Val Ile Gly Asp Phe Lys Val Val Gly Thr Gly Phe
            115                 120                 125
Pro Glu Asp Ser Val Ile Phe Thr Asp Lys Ile Ile Arg Ser Asn Ala
            130                 135                 140
```

```
Thr Val Glu His Leu His Pro Met Gly Asp Asn Val Leu Val Gly Ser
145                 150                 155                 160
Phe Ala Arg Thr Phe Ser Leu Arg Asp Gly Gly Tyr Tyr Ser Phe Val
                165                 170                 175
Val Asp Ser His Met His Phe Lys Ser Ala Ile His Pro Ser Ile Leu
                180                 185                 190
Gln Asn Gly Gly Pro Met Phe Ala Phe Arg Arg Val Glu Glu Leu His
                195                 200                 205
Ser Asn Thr Glu Leu Gly Ile Val Glu Tyr Gln His Ala Phe Lys Thr
                210                 215                 220
Pro Ile Ala Phe Ala Arg Ser Arg Ala Gln Ala Ser Asn Ser Ala Val
225                 230                 235                 240
Asp Gly Thr Ala Gly Pro Gly Ser Ala Ala Thr Leu Asp His Asn Gln
                245                 250                 255
Pro Tyr His Ile Cys Arg Gly Phe Thr Cys Phe Lys Lys Pro Pro Thr
                260                 265                 270
Pro Pro Pro Glu Pro Glu Thr
                275
```